

5/20 #4



OIPE

RAW SEQUENCE LISTING

DATE: 04/07/2003

PATENT APPLICATION: US/09/882,227

TIME: 09:47:31

Input Set : N:\vernette\US09882227.raw

Output Set: N:\CRF4\04072003\I882227.raw

1 <110> APPLICANT: Kleanthous, Harold
 2 Al-Garawi, Amal
 3 Miller, Charles
 4 Tomb, Jean-Francois
 5 Oomen, Raymond P.
 6 <120> TITLE OF INVENTION: Identification of Polynucleotides
 7 Encoding Novel Helicobacter Polypeptides in the Helicobacter
 8 Genome
 9 <130> FILE REFERENCE: 06132/047002
 10 <140> CURRENT APPLICATION NUMBER: US/09/882,227
 11 <141> CURRENT FILING DATE: 2001-06-15
 12 <150> PRIOR APPLICATION NUMBER: US 08/902,615
 13 <151> PRIOR FILING DATE: 1997-07-29
 14 <160> NUMBER OF SEQ ID NOS: 638
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1613
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Helicobacter pylori
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (64)...(1551)
 24 <400> SEQUENCE: 1

25	taagaaaaaac cgctagagtg caatacaatt cttgaaagat atgaaattaa aaaaggagac	60
26	ttt atg tta aaa atc aaa tta gaa aaa acc act ttt gaa aac gca aaa	108
27	Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys	
28	1 5 10 15	
29	gct gaa tgc agt tta gtt ttt att atc aat aag gat ttt agc cac gct	156
30	Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala	
31	20 25 30	
32	tgg gtc aaa aat aaa gag ttg cta gaa acc ttt aaa tac gaa ggc gaa	204
33	Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu	
34	35 40 45	
35	ggc gta ttt tta gac caa gaa aat aaa atc ctg tat gcg ggc gtt aaa	252
36	Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys	
37	50 55 60	
38	gaa gat gat gtg cat tta ttg aga gag agc gcg tgt tta gcc gtt cgc	300
39	Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg	
40	65 70 75	
41	acc ctt aaa aaa ctc gct ttt aaa agc gtt aaa gtg ggc gtt tat act	348
42	Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys Val Gly Val Tyr Thr	
43	80 85 90 95	
44	tgt ggt gca cat tct aaa gat aac gcg ctt tta gaa aac ttg aaa gcg	396

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45	Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu Glu Asn Leu Lys Ala	
46	100 105 110	
47	ctg ttt ttg ggc ttg aaa tta ggt ttg tat gaa tac gac act ttt aaa	444
48	Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu Tyr Asp Thr Phe Lys	
49	115 120 125	
50	tcc aac aaa aaa gaa agc gtt tta aaa gaa gcc att gtc gct tta gaa	492
51	Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala Ile Val Ala Leu Glu	
52	130 135 140	
53	ttg cac aaa cct tgc gaa aaa act tgc gca aat tct tta gaa aag agt	540
54	Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn Ser Leu Glu Lys Ser	
55	145 150 155	
56	gct aaa gaa gcg tta aaa tac gct gaa atc atg aca gaa agc ttg aat	588
57	Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met Thr Glu Ser Leu Asn	
58	160 165 170 175	
59	atc gtt aaa gat cta gtc aat acc ccc cct atg att ggc act ccg gtt	636
60	Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met Ile Gly Thr Pro Val	
61	180 185 190	
62	tat atg gct gaa gtg gcg caa aaa gtg gct aaa gaa aac cat tta gaa	684
63	Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys Glu Asn His Leu Glu	
64	195 200 205	
65	atc cat gtt cat gat gaa aaa ttt tta gaa gaa aag aaa atg aac gcc	732
66	Ile His Val His Asp Glu Lys Phe Leu Glu Glu Lys Lys Met Asn Ala	
67	210 215 220	
68	ttt tta gcg gtc aat aaa gcc tct ctt agc gtc aat cct cct cgc ttg	780
69	Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val Asn Pro Pro Arg Leu	
70	225 230 235	
71	atc cat tta gtc tat aag cct aaa aaa gcg aag aaa aaa atc gct tta	828
72	Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys Lys Lys Ile Ala Leu	
73	240 245 250 255	
74	gtg ggt aag ggc ttg act tat gat tgt ggg ggt ttg agc ttg aaa ccg	876
75	Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly Leu Ser Leu Lys Pro	
76	260 265 270	
77	gcc gat tac atg gtt act atg aaa gcg gat aaa ggc ggt ggc tct gcg	924
78	Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys Gly Gly Gly Ser Ala	
79	275 280 285	
80	gtg att ggg ctt tta aac gca tta gcc aaa cta ggc gtg gag gct gaa	972
81	Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu Gly Val Glu Ala Glu	
82	290 295 300	
83	gtg cat ggc att att ggg gct aca gaa aac atg ata ggc cca gcc gct	1020
84	Val His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala	
85	305 310 315	
86	tat aaa cca gat gat att ttg atc tcc aaa gaa ggc aag agc ata gag	1068
87	Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu	
88	320 325 330 335	
89	gtc cgt aat acc gac gct gag ggg cgt ttg gtt tta gcg gat tgt ttg	1116
90	Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu	
91	340 345 350	
92	agc tac gct caa gat tta aac cct gat gtg atc gtg gat ttt gcg acc	1164
93	Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr	

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```

94          355          360          365
95   ctt act ggg gca tgc gtt gta ggc tta ggc gaa ttc act tca gcg atc   1212
96   Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile
97          370          375          380
98   atg ggg cat aat gaa gag tta aaa aac ctc ttt gaa act tca ggg tta   1260
99   Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu
100          385          390          395
101   gaa tcc ggc gaa tta tta gcc aaa ctc ccc ttt aac cgc cat tta aag   1308
102   Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys
103   400          405          410          415
104   aaa ttg att gaa tct aaa atc gct gat gtg tgc aat att tct tct tca   1356
105   Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser
106          420          425          430
107   cgc tat ggc ggt gcg atc aca gcg ggc ttg ttt tta aat gaa ttt att   1404
108   Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile
109          435          440          445
110   aga gat gag ttt aag gat aag tgg cta cac att gac att gca ggc cct   1452
111   Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro
112   450          455          460
113   gct tat gtg gaa aaa gaa tgg gat gtg aat agc ttt gga gcg agt ggg   1500
114   Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly
115   465          470          475
116   gct ggc gtg aga gct tgc aca gct ttt gtg gaa gag ctt ttg aaa aag   1548
117   Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys
118   480          485          490          495
119   gct tgaaatgggc ttgtctgtag gcattgtggg tttgcctaata gtgggcaaata   1601
120   Ala
121   ccagcacctt ta   1613
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 496
125 <212> TYPE: PRT
126 <213> ORGANISM: Helicobacter pylori
127 <400> SEQUENCE: 2
128   Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys Ala
129   1          5          10          15
130   Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala Trp
131          20          25          30
132   Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu Gly
133          35          40          45
134   Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys Glu
135   50          55          60
136   Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg Thr
137   65          70          75          80
138   Leu Lys Lys Leu Ala Phe Lys Ser Val Lys Val Gly Val Tyr Thr Cys
139          85          90          95
140   Gly Ala His Ser Lys Asp Asn Ala Leu Leu Glu Asn Leu Lys Ala Leu
141          100          105          110
142   Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu Tyr Asp Thr Phe Lys Ser
143          115          120          125

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144 Asn Lys Lys Glu Ser Val Leu Lys Glu Ala Ile Val Ala Leu Glu Leu
145      130      135      140
146 His Lys Pro Cys Glu Lys Thr Cys Ala Asn Ser Leu Glu Lys Ser Ala
147      145      150      155      160
148 Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met Thr Glu Ser Leu Asn Ile
149      165      170      175
150 Val Lys Asp Leu Val Asn Thr Pro Pro Met Ile Gly Thr Pro Val Tyr
151      180      185      190
152 Met Ala Glu Val Ala Gln Lys Val Ala Lys Glu Asn His Leu Glu Ile
153      195      200      205
154 His Val His Asp Glu Lys Phe Leu Glu Glu Lys Lys Met Asn Ala Phe
155      210      215      220
156 Leu Ala Val Asn Lys Ala Ser Leu Ser Val Asn Pro Pro Arg Leu Ile
157      225      230      235      240
158 His Leu Val Tyr Lys Pro Lys Lys Ala Lys Lys Lys Ile Ala Leu Val
159      245      250      255
160 Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly Leu Ser Leu Lys Pro Ala
161      260      265      270
162 Asp Tyr Met Val Thr Met Lys Ala Asp Lys Gly Gly Gly Ser Ala Val
163      275      280      285
164 Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu Gly Val Glu Ala Glu Val
165      290      295      300
166 His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala Tyr
167      305      310      315      320
168 Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu Val
169      325      330      335
170 Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu Ser
171      340      345      350
172 Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr Leu
173      355      360      365
174 Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile Met
175      370      375      380
176 Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu Glu
177      385      390      395      400
178 Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys Lys
179      405      410      415
180 Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser Arg
181      420      425      430
182 Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile Arg
183      435      440      445
184 Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro Ala
185      450      455      460
186 Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly Ala
187      465      470      475      480
188 Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys Ala
189      485      490      495
191 <210> SEQ ID NO: 3
192 <211> LENGTH: 560
193 <212> TYPE: DNA

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194 <213> ORGANISM: Helicobacter pylori
195 <220> FEATURE:
196 <221> NAME/KEY: CDS
197 <222> LOCATION: (49)...(492)
198 <400> SEQUENCE: 3
199     ggcgaaatcg ggtaaatttt agcagggatt gccagctata ccggtcat atg cat tta 57
200                                     Met His Leu
201                                     1
202     ggg tta gcc att tta gtc gca ggg att ggg ggc ttt gtg ggg gat cag 105
203     Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val Gly Asp Gln
204         5             10             15
205     atc tat ttt tac atc ggc cgc acc aat aaa gct tac atc caa aaa aag 153
206     Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile Gln Lys Lys
207         20             25             30             35
208     cta gaa aaa caa cgc cga aaa cta gcc cta gcc cat tta ttg ttg caa 201
209     Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu Leu Leu Gln
210             40             45             50
211     aaa cac ggc tgg ttt atc att ttt atc caa cgc tat atg tat ggc atg 249
212     Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met Tyr Gly Met
213             55             60             65
214     cgc acc atc att ccc att agc ata ggt ctc acg cgt tat agc gct tta 297
215     Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr Ser Ala Leu
216             70             75             80
217     aaa ttc gct atc atc aat ctc att agc gcg atg gtg tgg gcg agc att 345
218     Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp Ala Ser Ile
219             85             90             95
220     acc att att cta gcg tgg tat tta gga gaa gag tta ttg cat gcg tta 393
221     Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Leu Leu His Ala Leu
222     100             105             110             115
223     ggg tgg ctt aaa aaa cac cct tat gcg cta ata tta cta tta gta tct 441
224     Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu Leu Val Ser
225             120             125             130
226     ttc ttg gcg tta gtg ctg tgg tat ttc caa tac tat agt aag aaa aac 489
227     Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser Lys Lys Asn
228             135             140             145
229     cgc tagagtgcaa tacaattcctt gaaagatatg aaattaaaaa aggagacttt 542
230     Arg
231     atgttaaaaa tcaaatta 560
233 <210> SEQ ID NO: 4
234 <211> LENGTH: 148
235 <212> TYPE: PRT
236 <213> ORGANISM: Helicobacter pylori
237 <400> SEQUENCE: 4
238     Met His Leu Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val
239         1             5             10             15
240     Gly Asp Gln Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile
241             20             25             30
242     Gln Lys Lys Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu
243             35             40             45

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; N Pos. 42,47
Seq#:27; N Pos. 920
Seq#:27; Xaa Pos. 301
Seq#:28; Xaa Pos. 301
Seq#:77; Xaa Pos. 304
Seq#:78; Xaa Pos. 304
Seq#:81; Xaa Pos. 32
Seq#:82; Xaa Pos. 32
Seq#:85; N Pos. 495
Seq#:86; Xaa Pos. 153
Seq#:103; N Pos. 71
Seq#:103; Xaa Pos. 17
Seq#:104; Xaa Pos. 17
Seq#:127; Xaa Pos. 6
Seq#:128; Xaa Pos. 6
Seq#:137; Xaa Pos. 12
Seq#:138; Xaa Pos. 12
Seq#:139; N Pos. 479,480,481,482,483
Seq#:139; Xaa Pos. 146,147,148
Seq#:140; Xaa Pos. 146,147,148
Seq#:143; N Pos. 9,12
Seq#:144; Xaa Pos. 3,4
Seq#:145; N Pos. 976,979
Seq#:145; Xaa Pos. 315,316
Seq#:146; Xaa Pos. 315,316
Seq#:153; N Pos. 409,457
Seq#:153; Xaa Pos. 128,144
Seq#:154; Xaa Pos. 128,144
Seq#:165; N Pos. 1028
Seq#:166; Xaa Pos. 326
Seq#:171; N Pos. 48
Seq#:171; Xaa Pos. 8
Seq#:172; Xaa Pos. 8
Seq#:277; Xaa Pos. 81
Seq#:278; Xaa Pos. 81
Seq#:305; N Pos. 388
Seq#:305; Xaa Pos. 118
Seq#:306; Xaa Pos. 118
Seq#:401; Xaa Pos. 217
Seq#:402; Xaa Pos. 217
Seq#:425; Xaa Pos. 182
Seq#:426; Xaa Pos. 182
Seq#:461; N Pos. 375
Seq#:461; Xaa Pos. 123

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Input Set : N:\vernette\US09882227.raw

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Seq#:462; Xaa Pos. 123
Seq#:553; N Pos. 528
Seq#:553; Xaa Pos. 172
Seq#:554; Xaa Pos. 172
Seq#:585; Xaa Pos. 66
Seq#:586; Xaa Pos. 66,102
Seq#:589; Xaa Pos. 171

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Input Set : N:\vernette\US09882227.raw

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L:1033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:915
M:341 Repeated in SeqNo=27
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:288
L:4099 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:77
L:4099 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:963
L:4233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:288
L:4414 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:81
L:4414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:150
L:4453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:16
L:4649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:486
L:4687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:144
L:5530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:51
M:341 Repeated in SeqNo=103
L:5622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:16
L:6938 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:127
L:6938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:51
L:6998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0
L:7439 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:137
L:7439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:158
L:7503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0
L:7581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:440
M:341 Repeated in SeqNo=139
L:7661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:144
L:7803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0
L:7859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:0
L:7962 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145 after pos.:966
M:341 Repeated in SeqNo=145
L:8014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:304
L:8269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:153 after pos.:390
M:341 Repeated in SeqNo=153
L:8300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154 after pos.:112
M:341 Repeated in SeqNo=154
L:8829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165 after pos.:1016
L:8889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:166 after pos.:320
L:9044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:171 after pos.:0
M:341 Repeated in SeqNo=171
L:9106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172 after pos.:0
L:15077 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:277
L:15077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:277 after pos.:294
L:15149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:278 after pos.:80
L:16693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:305 after pos.:342
M:341 Repeated in SeqNo=305
L:16750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:306 after pos.:112
L:22420 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:401
L:22420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:401 after pos.:675
L:22480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:402 after pos.:208
L:23803 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:425

VERIFICATION SUMMARY

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Input Set : N:\vernette\US09882227.raw

Output Set: N:\CRF4\04072003\I882227.raw

L:23803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:425 after pos.:582
L:23841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:426 after pos.:176
L:25953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:461 after pos.:337
M:341 Repeated in SeqNo=461
L:26065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:462 after pos.:112
L:31225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:537,Line#:0
L:32226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:553 after pos.:482
M:341 Repeated in SeqNo=553
L:32272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:554 after pos.:160
L:34202 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:585
L:34202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:585 after pos.:243
L:34339 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:589